

## FINGERPRINTING OF COMMON BEAN GENOTYPES

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Progress in molecular genetic techniques provide us with new tools to characterize genetic diversity among organisms. These tools can be used for a variety of purposes: fingerprinting of cultivars; detection of duplicates in germplasm collections; characterization of population genetic structure of wild and landrace populations; monitoring of introgression of traits from exotic into adapted genetic backgrounds; and genetic linkage analysis.

Here, we present some of these new tools and discuss their relative merits in characterizing genetic diversity.

### 1. Minisatellite sequences:

Sequences such as the tandem repeat of the M13 protein III gene and the human minisatellite sequences have been reported to hybridize to plant sequences (Dallas 1988; Rogstad et al. 1988). After preliminary experiments confirmed that these sequences also hybridized to common bean DNA, we addressed the following issues:

#### Level of environmental and generational stability

DNA was extracted from leaf samples of pink bean cultivar 'Yolano' plants, grown in 4 different locations around Davis, CA, and analyzed after hybridization with M13. Results showed a uniform pattern suggesting that: 1) the banding pattern is constant irrespective of the environment; and 2) the characteristic banding pattern has remained constant in spite of several generations of seed increase during the certification process.

#### Level of variability

Different materials have been analyzed with M13. These include: 1) wild forms and landraces from Latin America representing the various common bean races (Singh et al. 1991); and 2) California cultivars.

Results show that wild forms and landraces display a substantial amount of variation (even among geographically or racially related materials) but that the California cultivars tend to be homogeneous within commercial market classes, especially among the kidneys and the pinks. More than one fingerprinting sequence appears to be necessary to distinguish these closely related materials.

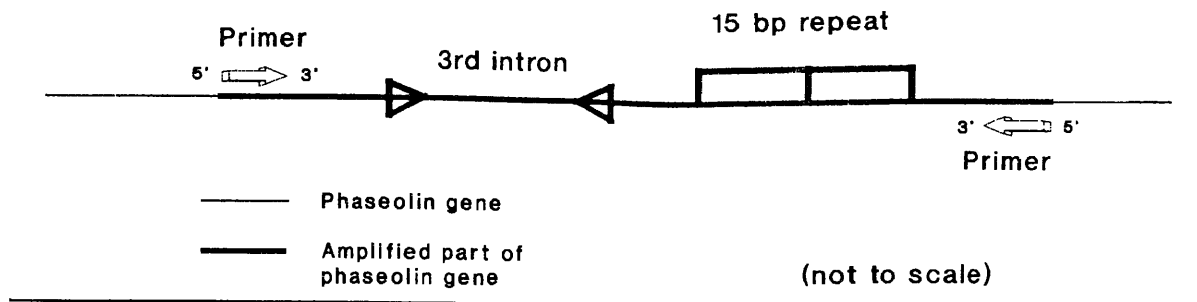
### 2. Polymerase chain reaction (PCR):

PCR requires sequence information to devise two sequences approximately 20 nucleotides long that can act as primers for the DNA polymerase enzyme. Once adequate primers have been devised, PCR allows rapid amplification of the sequence included between the two primers. We have developed 2 primers that allow us to distinguish the Middle American and Andean phaseolin types. These two primers flank the 15 base pair repeat and the third intron.

### 3. Randomly amplified polymorphic DNA (RAPDs):

RAPDs were initially proposed by Williams et al. (1990) and Welsh and McClelland (1990). We have been able to adapt RAPD markers for common bean in a reproducible way. Advantages include their speed (no Southern hybridization) and lack of radioisotope use. Disadvantages include sensitivity to experimental conditions and

## Gene pool specific phaseolin fingerprinting



**Figure 6.** Location of primers for amplification of gene pool-specific sequences of the phaseolin gene.

reduction in statistical power in segregation and linkage analyses when dealing with heterozygotes.

#### 4. *Pst*I genomic clones:

Among the 10 % of the clones in a *Pst*I genomic library that detects single copy sequences (Nodari et al. n.d.), some clones revealed complex banding patterns when hybridized to genomic DNA.

The major advantage of molecular markers is that they reflect genetic relatedness more accurately than phenotypic markers. Their major disadvantage is that their relationship with agronomic traits, if any, needs to be determined. The relative merits of various molecular markers can be assessed using various parameters: level of polymorphism, environmental and experimental stability, number of loci, molecular basis of polymorphism, and practicality. Depending on the objective of the analysis, one or the other or specific combinations of markers can be used.

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